

0340/0590



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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/944,049

DATE: 03/06/2002
 TIME: 13:04:54

Input Set : A:\-25-1.app
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3 <110> APPLICANT: Schall, Thomas J.
 4 Penfold, Mark E.T.
 5 ChemoCentryx, Inc.
 7 <120> TITLE OF INVENTION: Inhibition of CMV Infection and Dissemination
 9 <130> FILE REFERENCE: 019934-002510US
 11 <140> CURRENT APPLICATION NUMBER: US 09/944,049
 12 <141> CURRENT FILING DATE: 2001-08-30
 14 <150> PRIOR APPLICATION NUMBER: US 60/229,365
 15 <151> PRIOR FILING DATE: 2000-08-30
 17 <160> NUMBER OF SEQ ID NOS: 48
 19 <170> SOFTWARE: PatentIn Ver. 2.1
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 22 <211> LENGTH: 1065
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Human cytomegalovirus
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: human cytomegalovirus (HCMV) Toledo strain open
 28 reading frame US28 (AU4.1)
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
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 33 <223> OTHER INFORMATION: HCMV Toledo US28
 35 <400> SEQUENCE: 1
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 38 ggcgttgcgtt ttctgttcgg ttccatcgcc aacttcttgg tgatcttcac catcacctgg 180
 39 cgacgtcgga ttcaatgctc cggcgatgtt tactttatca acctcgccgc cgccgatttg 240
 40 cttttcggtt gtacactacc tctgtggatg caataacctcc tagatcacaa ctcccttagcc 300
 41 agcgtgcgtt gtacgttact cactgcctgt ttctacgtgg ctatgtttgc cagtttgcgt 360
 42 tttatcacgg agattgcact cgatcgctac tacgctattt tttacatgag atatcgccct 420
 43 gtaaaacagg cctgcctttt cagtattttt tggtgatct ttgccgtat catcgccatt 480
 44 ccacattttt tggtggtgac caaaaaagac aatcaatgta tgaccgacta cgactactta 540
 45 gaggtcagct acccgatcat cctcaacgta gaactcatgc tcgggtcgtt cgtgatcccg 600
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 48 tggctgcgtt accacctaaccgttgcgtt gacacgttacaa aactcctcaa atggatctcc 780
 49 agcagctgcg agttcgaaag atcgctcaaa cgtgcgtca tcttgaccga gtcgctcgcc 840
 50 ttttgcgttact gttgtctcaa tccgctgtt tacgtcttcg tgggcaccaa gtttcggcaa 900
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 52 taccacagca ttagctttc gcgtcgagc tcgcccggcc gaagagagagac atcttccgac 1020
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58 <212> TYPE: PRT
59 <213> ORGANISM: Human cytomegalovirus
61 <220> FEATURE:
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67 1 5 10 15
69 Asp Glu Ala Ala Thr Pro Cys Val Phe Thr Asp Val Leu Asn Gln Ser
70 20 25 30
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73 35 40 45
75 Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile
76 50 55 60
78 Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Ala Asp Leu
79 65 70 75 80
81 Leu Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His
82 85 90 95
84 Asn Ser Leu Ala Ser Val Pro Cys Thr Leu Leu Thr Ala Cys Phe Tyr
85 100 105 110
87 Val Ala Met Phe Ala Ser Leu Cys Phe Ile Thr Glu Ile Ala Leu Asp
88 115 120 125
90 Arg Tyr Tyr Ala Ile Val Tyr Met Arg Tyr Arg Pro Val Lys Gln Ala
91 130 135 140
93 Cys Leu Phe Ser Ile Phe Trp Trp Ile Phe Ala Val Ile Ile Ala Ile
94 145 150 155 160
96 Pro His Phe Met Val Val Thr Lys Lys Asp Asn Gln Cys Met Thr Asp
97 165 170 175
99 Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Ile Ile Leu Asn Val Glu Leu
100 180 185 190
102 Met Leu Gly Ala Phe Val Ile Pro Leu Ser Val Ile Ser Tyr Cys Tyr
103 195 200 205
105 Tyr Arg Ile Ser Arg Ile Val Ala Val Ser Gln Ser Arg His Lys Gly
106 210 215 220
108 Arg Ile Val Arg Val Leu Ile Ala Val Val Leu Val Phe Ile Ile Phe
109 225 230 235 240
111 Trp Leu Pro Tyr His Leu Thr Leu Phe Val Asp Thr Leu Lys Leu Leu
112 245 250 255
114 Lys Trp Ile Ser Ser Ser Cys Glu Phe Glu Arg Ser Leu Lys Arg Ala
115 260 265 270
117 Leu Ile Leu Thr Glu Ser Leu Ala Phe Cys His Cys Cys Leu Asn Pro
118 275 280 285
120 Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
121 290 295 300
123 Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
124 305 310 315 320
126 Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
127 325 330 335
129 Thr Ser Ser Asp Thr Leu Ser Asp Glu Val Cys Arg Val Ser Gln Ile

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142	reading frame US28		
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152	ggcggtgtct ttcttccgg ttccatcggc aacttcttgg ttagtcttacat catcacctgg 180		
153	cgacgtcgga ttcaatgttc cggcgatgtt tactttatca acctcgccgc cgccgatttg 240		
154	cttttcgttt gtacactacc tctgtggatg caatacctcc tagatcacaa ctccctagcc 300		
155	agcgtgccgt gtacgttact cactgcctgt ttctacgtgg ctatgttgc cagtttgtgt 360		
156	tttacacgg agattgcact cgatcgctac tacgctattt tttacatgag atatcgccct 420		
157	gtaaaaacagg cctgcctttt cagtattttt tggggatct ttgcgtgtat catcgccatt 480		
158	ccacacttta tgggtgtgac caaaaaagac aatcaatgtt tgaccgacta cgactactta 540		
159	gaggtcgtt acccgatcat cctcaacgtt gaactcatgc tcgggtcttt cgtgatcccg 600		
160	ctcagtgta tcagctactg ctactaccgc atttccagaa tcggtcggt gtctcagtcg 660		
161	cggcacaaag gccgcattgt acgggtactt atagcggtcg tgcttgcattt tattatcttt 720		
162	tggctgccgt accacactgac gctgtttgtt gacacgttga aactgctcaa atggatctcc 780		
163	agcagctcgccgt agttcgaaaa atcactcaag cgcgcgtca tcttgaccga gtcaactcgcc 840		
164	ttttgtcaact gttgtctcaa tccgctgtt tacgttgcgtt tgggcaccaa gtttcggcaa 900		
165	gaactgcact gtctgtggc cgagtttgcg cagcactgtt tttccgcga tttatcctgg 960		
166	taccacagca tgagcttttgcgttgcgtt tacgttgcgtt tgggcaccaa gtttcggcaa 1020		
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183	Asp Asp Glu Ala Thr Pro Cys Val Leu Thr Asp Val Leu Asn Gln Ser		
184	20 25 30		
186	Lys Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser		
187	35 40 45		
189	Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile		
190	50 55 60		
192	Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Asp Leu		

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195	Leu	Phe	Val	Cys	Thr	Leu	Pro	Leu	Trp	Met	Gln	Tyr	Leu	Leu	Asp	His
196					85					90					95	
198	Asn	Ser	Leu	Ala	Ser	Val	Pro	Cys	Thr	Leu	Leu	Thr	Ala	Cys	Phe	Tyr
199					100				105					110		
201	Val	Ala	Met	Phe	Ala	Ser	Leu	Cys	Phe	Ile	Thr	Glu	Ile	Ala	Leu	Asp
202					115				120					125		
204	Arg	Tyr	Tyr	Ala	Ile	Val	Tyr	Met	Arg	Tyr	Arg	Pro	Val	Lys	Gln	Ala
205					130				135					140		
207	Cys	Leu	Phe	Ser	Ile	Phe	Trp	Trp	Ile	Phe	Ala	Val	Ile	Ile	Ala	Ile
208	145					150					155				160	
210	Pro	His	Phe	Met	Val	Val	Thr	Lys	Lys	Asp	Asn	Gln	Cys	Met	Thr	Asp
211					165				170					175		
213	Tyr	Asp	Tyr	Leu	Glu	Val	Ser	Tyr	Pro	Ile	Ile	Leu	Asn	Val	Glu	Leu
214					180				185					190		
216	Met	Leu	Gly	Ala	Phe	Val	Ile	Pro	Leu	Ser	Val	Ile	Ser	Tyr	Cys	Tyr
217					195				200					205		
219	Tyr	Arg	Ile	Ser	Arg	Ile	Val	Ala	Val	Ser	Gln	Ser	Arg	His	Lys	Gly
220					210				215					220		
222	Arg	Ile	Val	Arg	Val	Leu	Ile	Ala	Val	Val	Leu	Val	Phe	Ile	Ile	Phe
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226					245					250				255		
228	Lys	Trp	Ile	Ser	Ser	Ser	Cys	Glu	Phe	Glu	Lys	Ser	Leu	Lys	Arg	Ala
229					260				265					270		
231	Leu	Ile	Leu	Thr	Glu	Ser	Leu	Ala	Phe	Cys	His	Cys	Cys	Leu	Asn	Pro
232					275				280					285		
234	Leu	Leu	Tyr	Val	Phe	Val	Gly	Thr	Lys	Phe	Arg	Gln	Glu	Leu	His	Cys
235					290				295					300		
237	Leu	Leu	Ala	Glu	Phe	Arg	Gln	Arg	Leu	Phe	Ser	Arg	Asp	Val	Ser	Trp
238	305					310					315				320	
240	Tyr	His	Ser	Met	Ser	Phe	Ser	Arg	Arg	Ser	Ser	Pro	Ser	Arg	Arg	Glu
241					325					330				335		
243	Thr	Ser	Ser	Asp	Thr	Leu	Ser	Asp	Glu	Ala	Cys	Arg	Val	Ser	Gln	Ile
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256		rhUS28.1														
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267 gcctctatgg ccgacactcg cagcaactgtc atgctaccgc tctggctaca ttatgtcctc 240
268 aactttgccc aactctctcg aggagcctgt atcagcttt cggtgacttt ctatgttccc 300
269 cttttcggtt aggccctgggtt actcatttcc atcgtatgg agcgatattc caacttagta 360
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290 rhUS28.1
292 <400> SEQUENCE: 6
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297 20 25 30
299 Gly Leu Val Gly Asn Leu Leu Cys Ile Val Leu Val Lys Lys Arg
300 35 40 45
302 Lys Leu Arg Tyr Ser Ser Asp Val Tyr Phe Phe His Ala Ser Met Ala
303 50 55 60
305 Asp Leu Val Ser Thr Val Met Leu Pro Leu Trp Leu His Tyr Val Leu
306 65 70 75 80
308 Asn Phe Ala Gln Leu Ser Arg Gly Ala Cys Ile Ser Phe Ser Val Thr
309 85 90 95
311 Phe Tyr Val Pro Leu Phe Val Gln Ala Trp Leu Leu Ile Ser Ile Ala
312 100 105 110
314 Met Glu Arg Tyr Ser Asn Leu Val Trp Met Ala Pro Ile Ser Val Lys
315 115 120 125
317 Thr Ala Phe Lys His Cys Ile Gly Thr Trp Ile Val Ser Ala Phe Val
318 130 135 140
320 Ala Ser Pro Tyr Tyr Ala Tyr Arg Asn Ser His Asp Glu His Glu Cys
321 145 150 155 160
323 Ile Leu Gly Asn Tyr Thr Trp His Ile Asn Glu Pro Leu His Thr Cys
324 165 170 175
326 Met Asp Val Val Ile Ile Val Trp Thr Phe Leu Ala Pro Val Leu Val
327 180 185 190
329 Thr Ile Ile Ala Ser Val Lys Met Arg Arg Thr Thr Trp Gly Asn Thr

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